

FIGURE 1

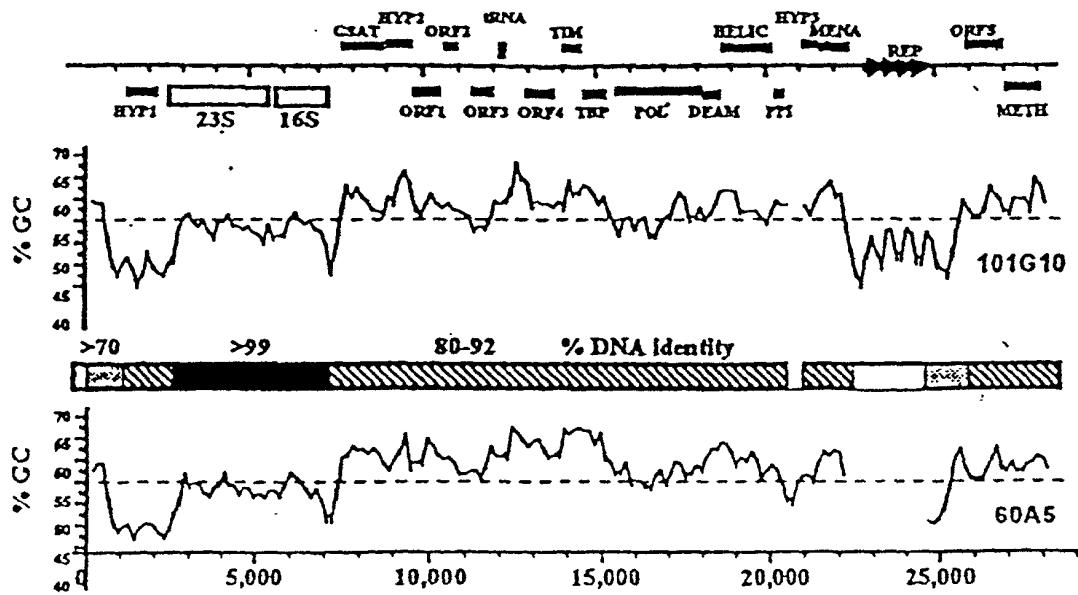


FIGURE 2

Seq ID No	Gene	Strain	TATA Box	Coding Start	TATA_to_Start (bp)
81	Hypoth 03	A	AAGCTAGACT TTTAAT TGGG ATCCGGCGGG GCGGCAGCATG	-----	25
82		B	AAGCTAAACT TTTAAT TGGG ATCCGGCGAG CCGGCAGCGTC	-----	
83	Hypoth 02	A	GGAAACTTGT ATTATA CGGG CGTGCTGCC CGGGGCCAT G	-----	26
84		B	GGAAACTTGT ATTATA CGGG CGTACATTCC CGGGGCCAT G	-----	
85	ORF 02	A	AAGGCAAGGT AATAAT AGCC TGCGCTGT AACGGCGTA TG	-----	27
86		B	ACGGCAAGGT AATAAT AGCC TGCGCTCGT ACCTGCGTA TG	-----	
87	ORF 03	A	CATGGAACTA GATATT AACC GGTTCCGCGG ATCCCAGTCA TG	-----	27
88		B	CATGGAACTA GATAAT AACC GGTCGGCGG GTACAATGCA TG	-----	
89	PPI	A	ATACCGAGAA GTTATA GCAG GGTATGAAAT GTGCGCGCG ATG	-----	28
90		B	AGCACGACAA GTTATA GCAG GGTACAAAGG AGCAGCGCAC ATG	-----	
91	GSAT	A	ATCCGCCCTG ATTAAA TTAT GGGGGGAGCG GCCTGCTGCC GTG	-----	28
92		B	ATCCGCCCTC ATTAAA TTAC GGGGGGTACA ACCTGCTGCC GTG	-----	
93	ORF 05	A	CCTTCATACA CATAAA TCCC GCTTGGATGT CGGGCTGCC ATG	-----	28
94		B	ACTTCATACA CATAAA TCCC GCCTGAACGG TCGTCCGCC ATG	-----	
95	deaminase	A	GGCATATAC CATAAT ATGC CGGGCGGTGG CACCATGCC GTG	-----	29
96		B	CCGCATATAC CATAAT ATGC CGGGCGGGGG CAGGCTGCC GTG	-----	
97	RNA helic	A	TGTACGAAAC CATAAA ACAA CAGGCCGCGT CAGGGCCGCG CGTG	-----	29
98		B	GGGTAGAAAC CATAAA ACAA CAGGCCGCGG CAGGGCG CG CGTG	-----	
99	ORF 06	A	ACACGGCAG TATAAA CGGG GGGCGGGCG GCGCGTATCA CATG	-----	29
100		B	ATACACGTGG TATAAA CAGA GG CGGAGC CGCCGGACCA CATG	-----	
101	tRNA-tyr	A	GCGATAGTTA TTTAAA ACTA GGATGCCGAT CACGGATCGT CCCA	-----	29
102		B	GCGATAGTTA TTTAAA ACTA GGATGCCGGG CACCCGTCGT CCCA	-----	
103	TBP	A	CCGGGCCCG GTTAAA ATAG CG CACGGGC GGATCCTGAC CAATG	-----	30
104		B	CCGGGCCCG GTTAAA ATAG AGTGGGGCGG CGCACCGGAT CAATG	-----	
105	TIM	A	GCGTCGATAG AATAAA TAGC CGCAGGGGGC CCCGTGGCG GATGCCCGT G	-----	36
106		B	GCGTCGATAG AATAAA TAGC CGC CGGGGC CGGGTGC... GATGCCCGT G	-----	
107	Hypoth 01	A	ATTTCAACTA CATAAA TGCC TAGTACGCA GAAATAGCAA ACGACGTACT TCGACTAATG	-----	45
108		B	ACTTCACACTA CATAAA TGCC TAGTACGCA GAAATATCAA ACAAAAGTACT TCGACTAATG	-----	
109	ORF 01	A	ACGGCAGGCT ATTATT ACCT TGCGCTGCGT TGTA //..G CGGGGTGCGG CAGGGGATG	-----	52
110		B	ACGGCAGGCT ATTATT ACCT TGCGCTGCGT TACA //..G AGGGGGCTG CGGGGAGTG	-----	
111	Methylase	A	CTACAACGAT TTTAAG TCGG CGGGGGGCA GCCG //..G ATGTGGGGCA GGCAACATG	-----	104
112		B	CTACAACGAT TTTAAG ACGG CGGGGGTGCC CGGG //..T GGCACGGGG CCTATCTTG	-----	
113	16S RNA	A	TCGGCGATGG TTTATA TGCC CATGGACGGG CCGATCCGAT CGTACGTGAC GC //..AAT	-----	220
114		B	CGGGCGATGG TTTATA TGCC CATGGACAAG GCGATCCGAT CGTACGTGAC GC //..AAT	-----	
Archaeal promoter consensus					
			YTTAWA		

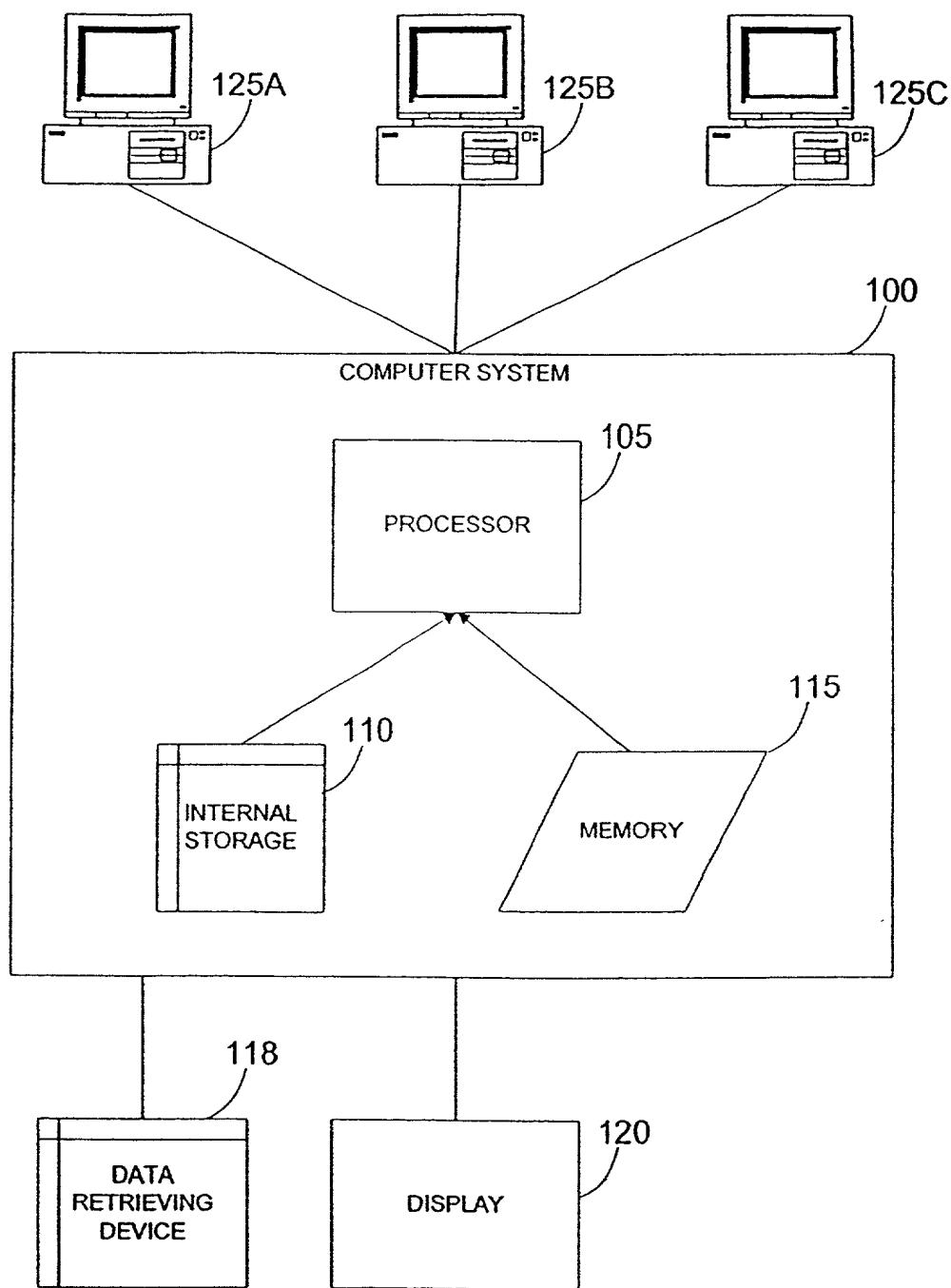


FIGURE 3

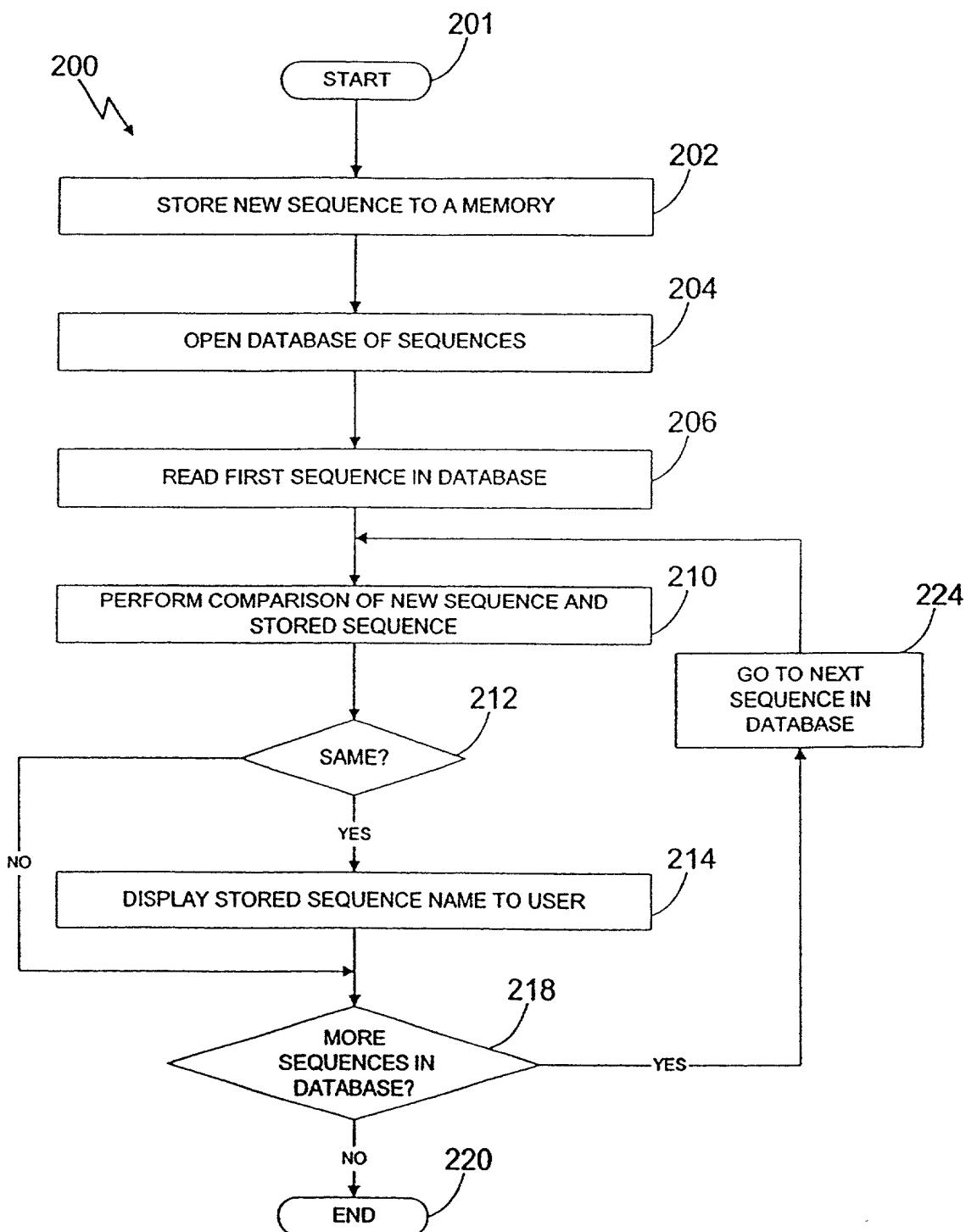


FIGURE 4

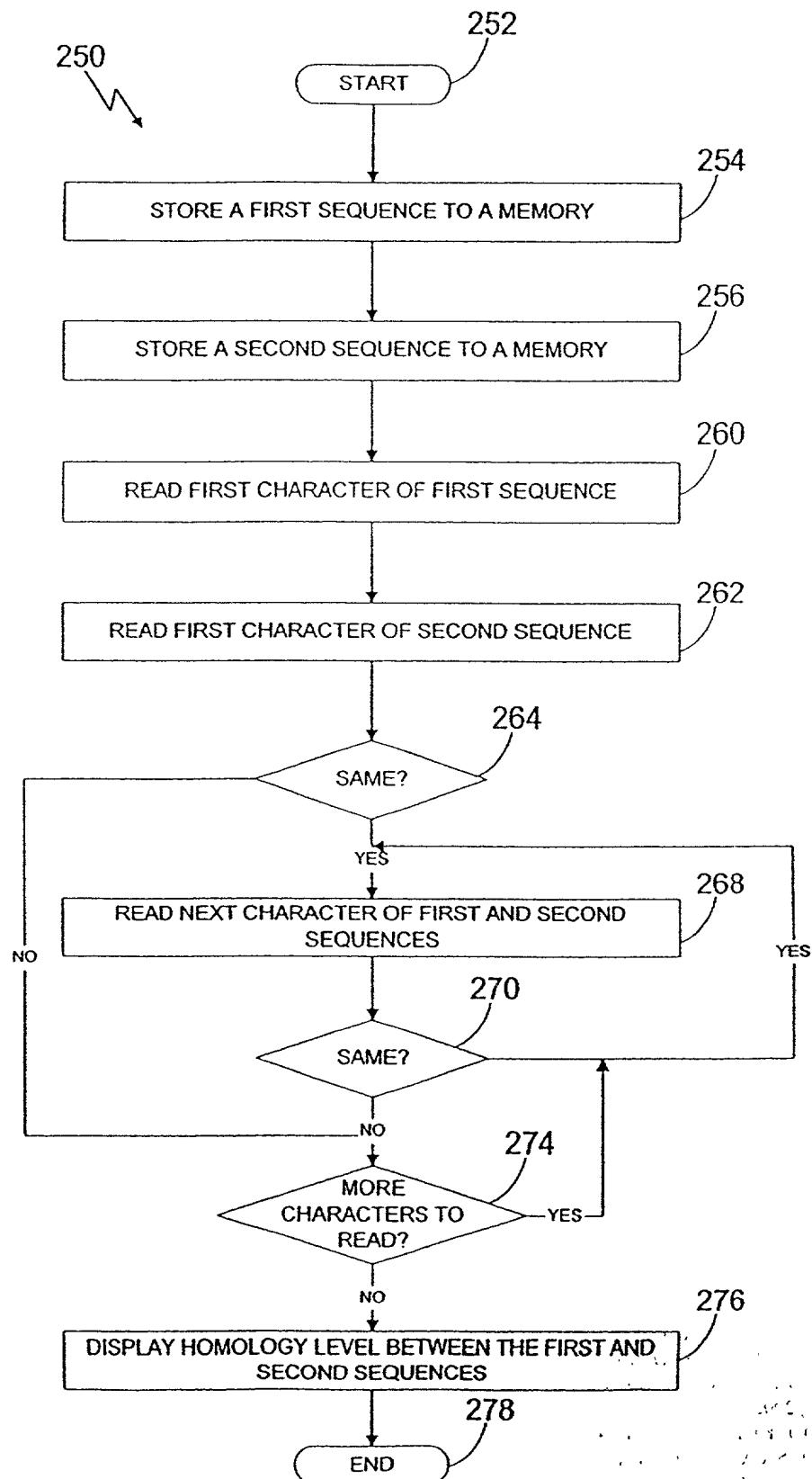


FIGURE 5

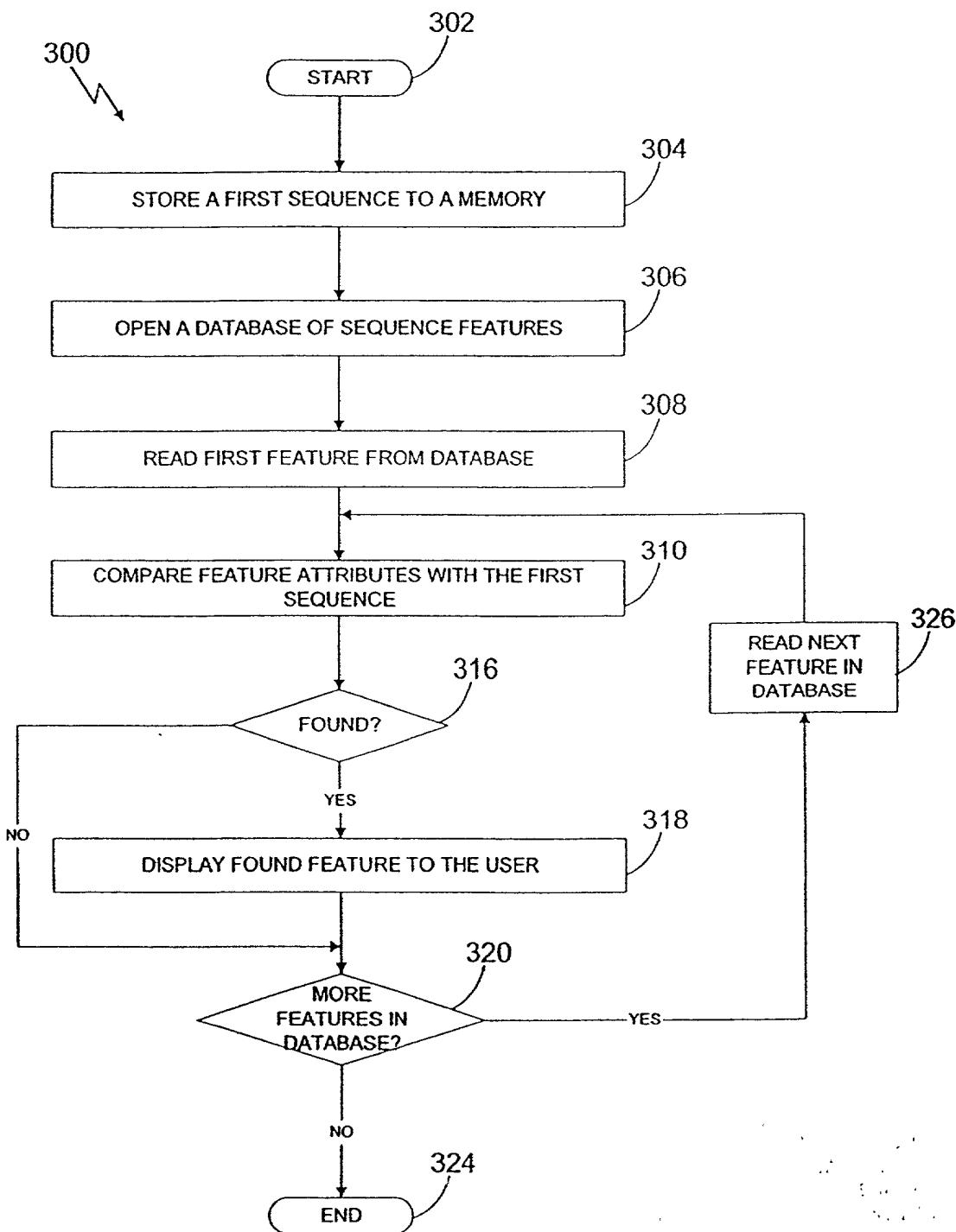


FIGURE 6